Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:23:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472380.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472380_1.fastq.gz SRR3472380_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:23:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,158,804
Mapped reads	19,008,804 / 99.22%
Unmapped reads	150,000 / 0.78%
Mapped paired reads	19,008,804 / 99.22%
Mapped reads, first in pair	9,528,002 / 49.73%
Mapped reads, second in pair	9,480,802 / 49.49%
Mapped reads, both in pair	18,918,506 / 98.75%
Mapped reads, singletons	90,298 / 0.47%
Secondary alignments	0
Supplementary alignments	66,757 / 0.35%
Read min/max/mean length	30 / 100 / 99.38
Duplicated reads (estimated)	12,018,096 / 62.73%
Duplication rate	47.37%
Clipped reads	1,320,473 / 6.89%

2.2. ACGT Content

Number/percentage of A's	498,255,905 / 26.73%
Number/percentage of C's	435,260,991 / 23.35%
Number/percentage of T's	499,138,095 / 26.78%
Number/percentage of G's	431,197,956 / 23.13%
Number/percentage of N's	230,723 / 0.01%

GC Percentage	46.48%

2.3. Coverage

Mean	0.6022
Standard Deviation	18.395

2.4. Mapping Quality

Mean Mapping Quality	54.91

2.5. Insert size

Mean	15,835.62
Standard Deviation	1,238,181.2
P25/Median/P75	152 / 210 / 281

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	10,054,298
Insertions	104,680
Mapped reads with at least one insertion	0.54%
Deletions	87,742
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.01%

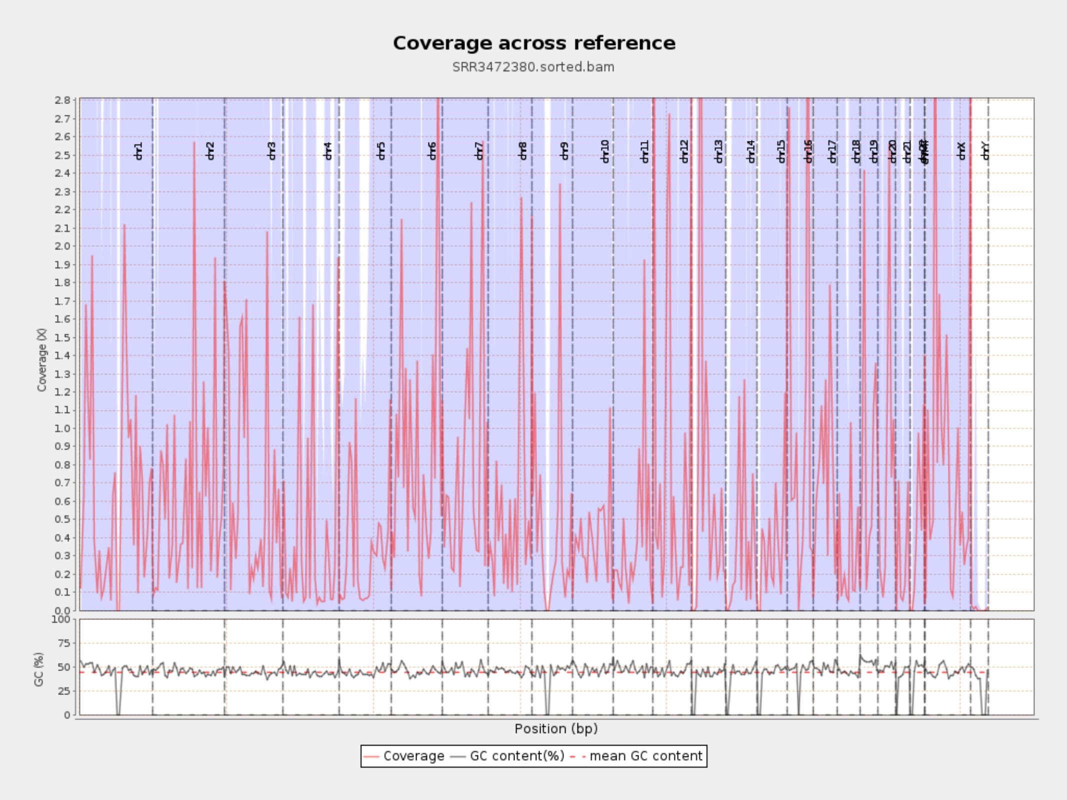
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

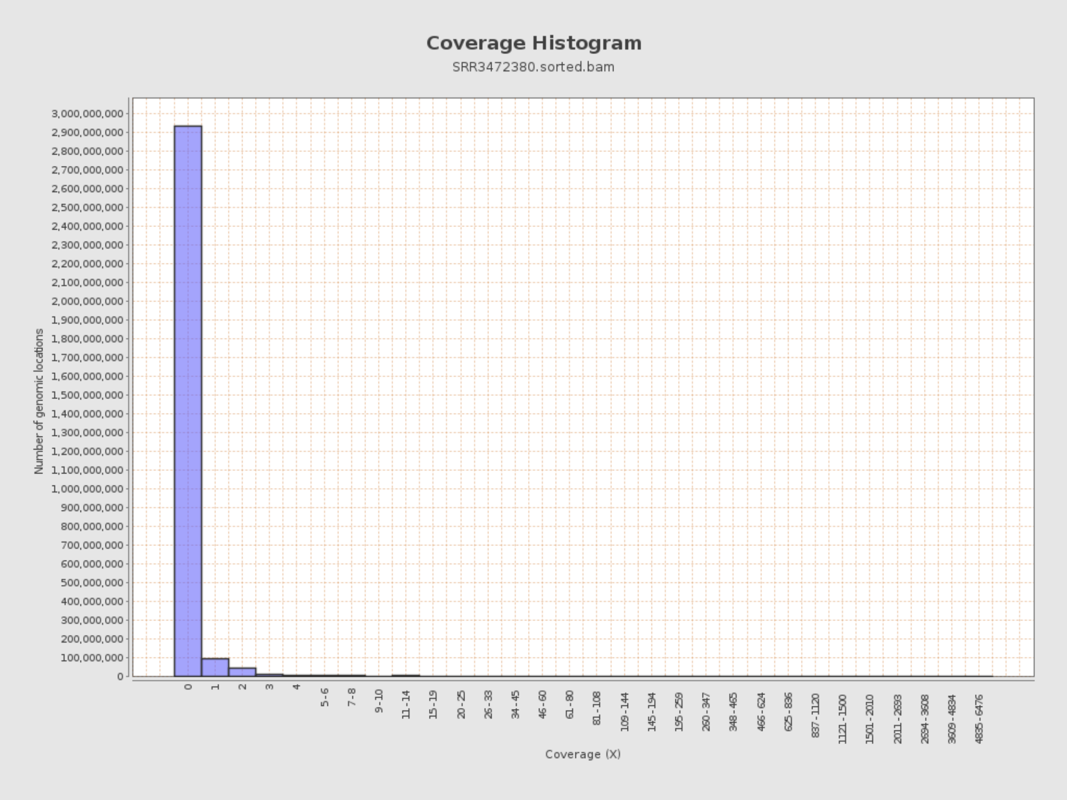
		bases	coverage	deviation
chr1	249250621	167204015	0.6708	19.501
chr2	243199373	147634394	0.6071	17.428
chr3	198022430	135456198	0.684	19.6292
chr4	191154276	73369349	0.3838	16.4993
chr5	180915260	62590997	0.346	10.913
chr6	171115067	149572502	0.8741	23.3457
chr7	159138663	133738766	0.8404	22.362
chr8	146364022	83279639	0.569	20.7793
chr9	141213431	65502969	0.4639	14.8662
chr10	135534747	53312055	0.3933	11.4623
chr11	135006516	53869290	0.399	14.5683
chr12	133851895	113166439	0.8455	21.8942
chr13	115169878	87302348	0.758	25.2232
chr14	107349540	37466738	0.349	12.1292
chr15	102531392	37389489	0.3647	13.0885
chr16	90354753	100703898	1.1145	31.4569
chr17	81195210	62473996	0.7694	14.9901
chr18	78077248	23459449	0.3005	11.1736
chr19	59128983	53886494	0.9113	20.9538
chr20	63025520	50725314	0.8048	19.9472
chr21	48129895	13802951	0.2868	12.2587
chr22	51304566	23871071	0.4653	15.5364
chrMT	16571	23307	1.4065	1.4558
chrX	155270560	133985374	0.8629	19.029

chrY	59373566	506048	0.0085	0.6583

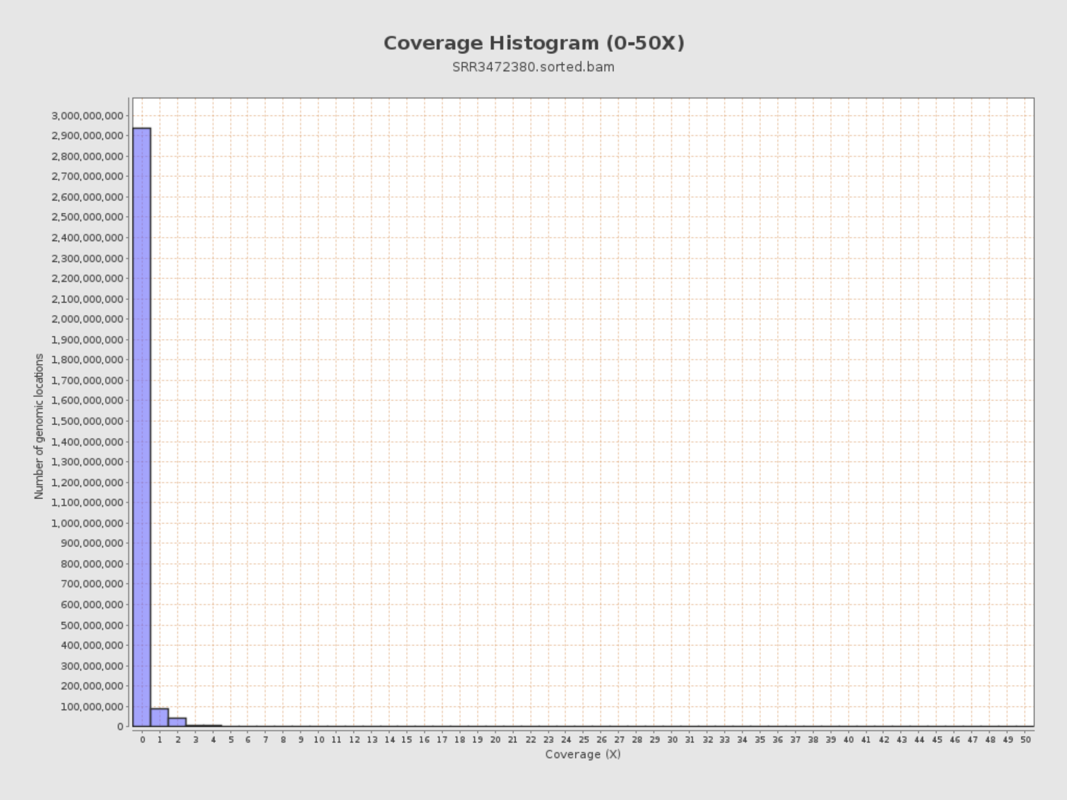
3. Results : Coverage across reference



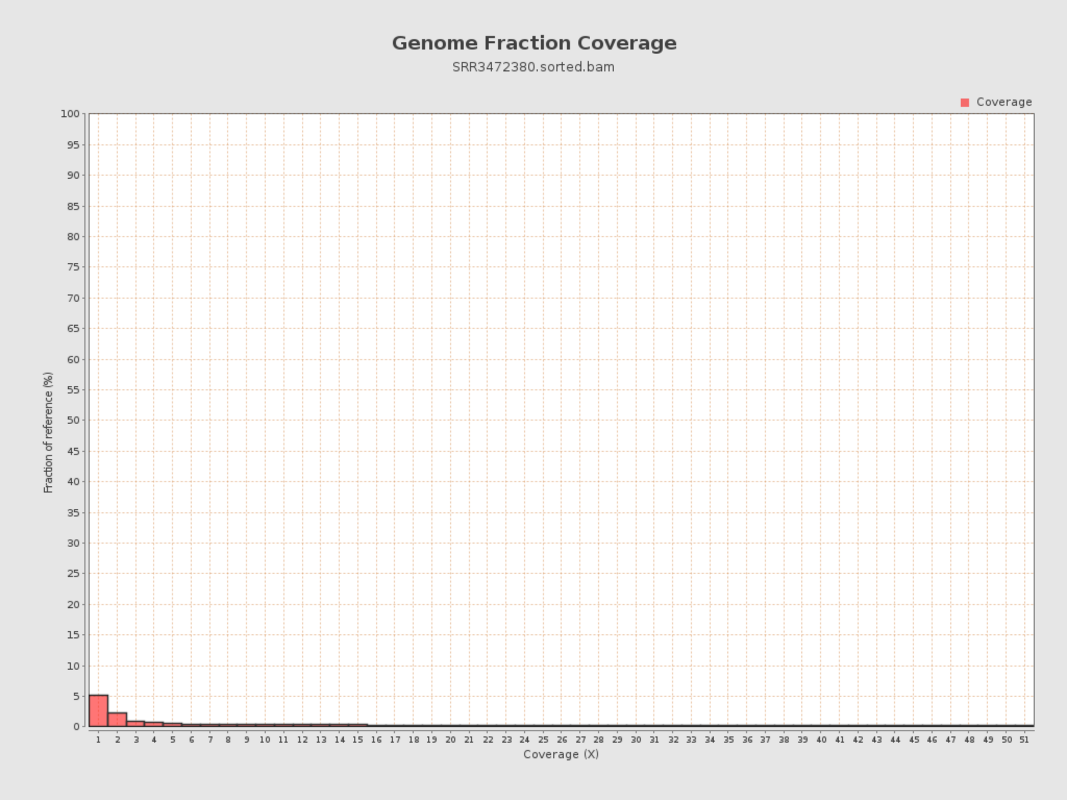
4. Results : Coverage Histogram



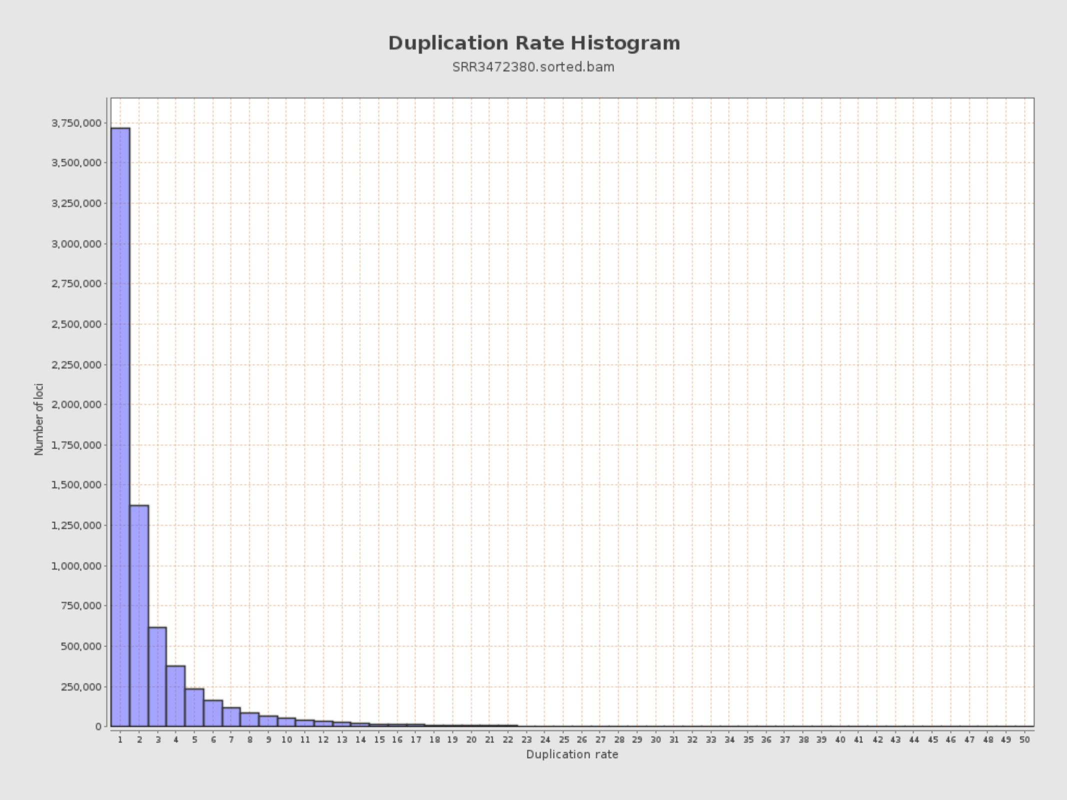
5. Results : Coverage Histogram (0-50X)



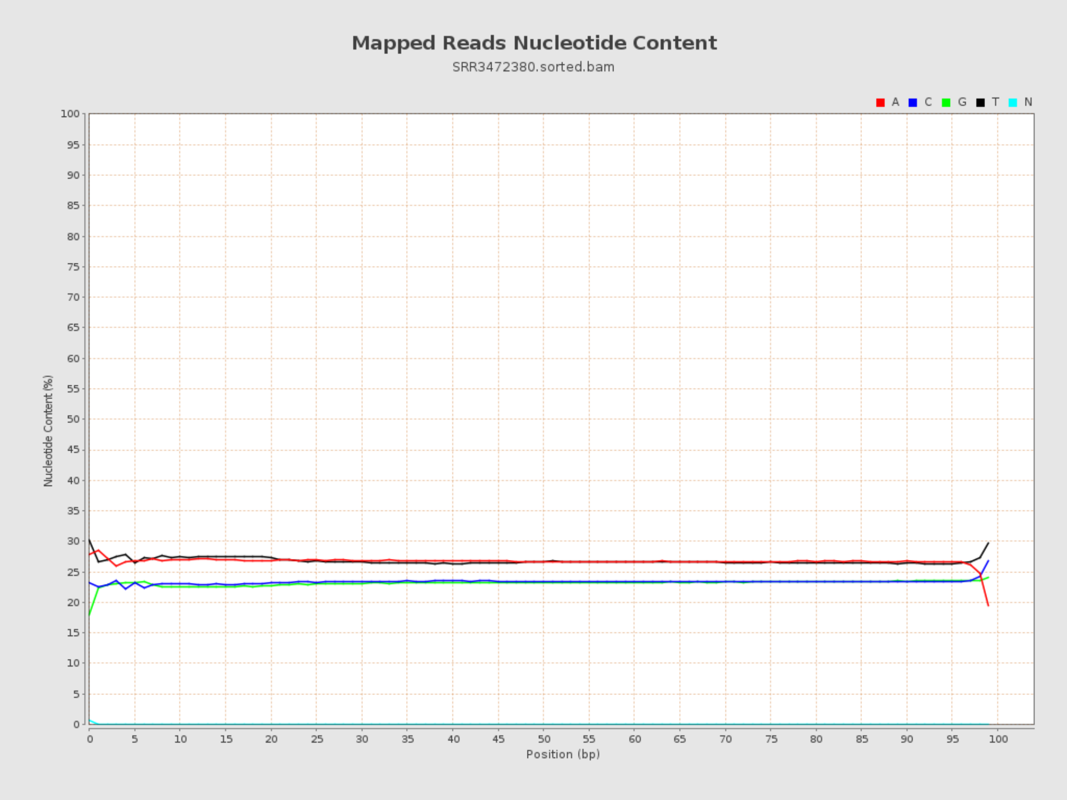
6. Results : Genome Fraction Coverage



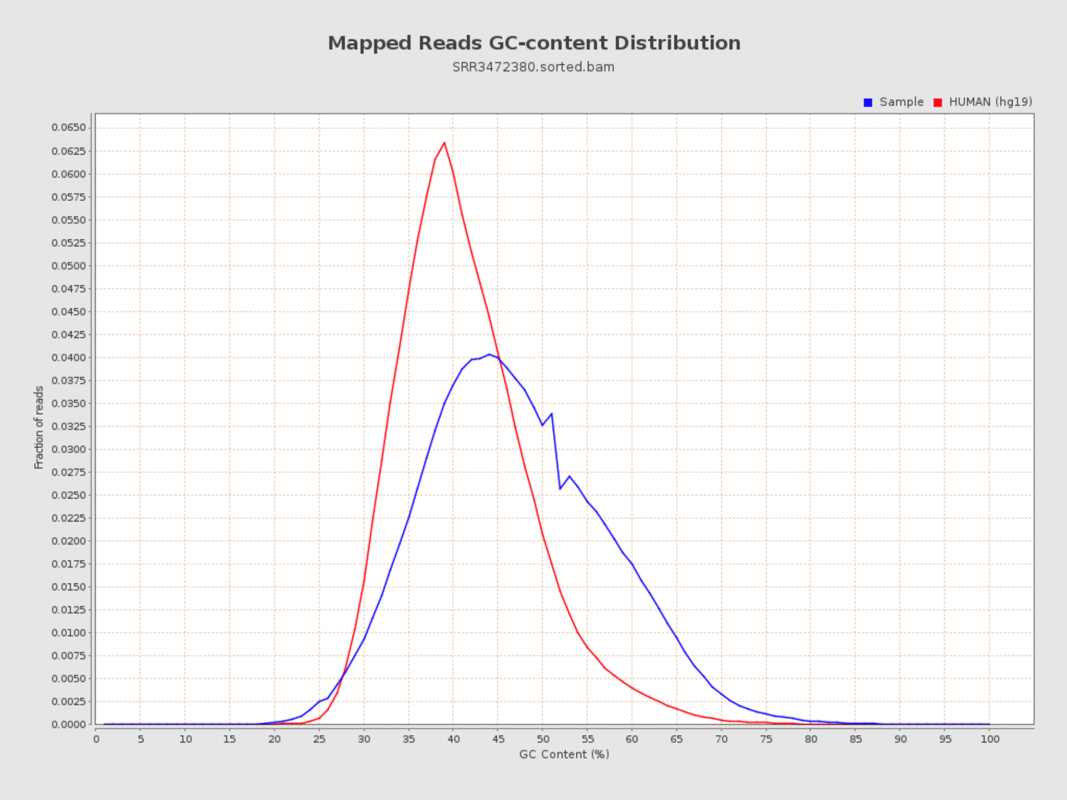
7. Results : Duplication Rate Histogram



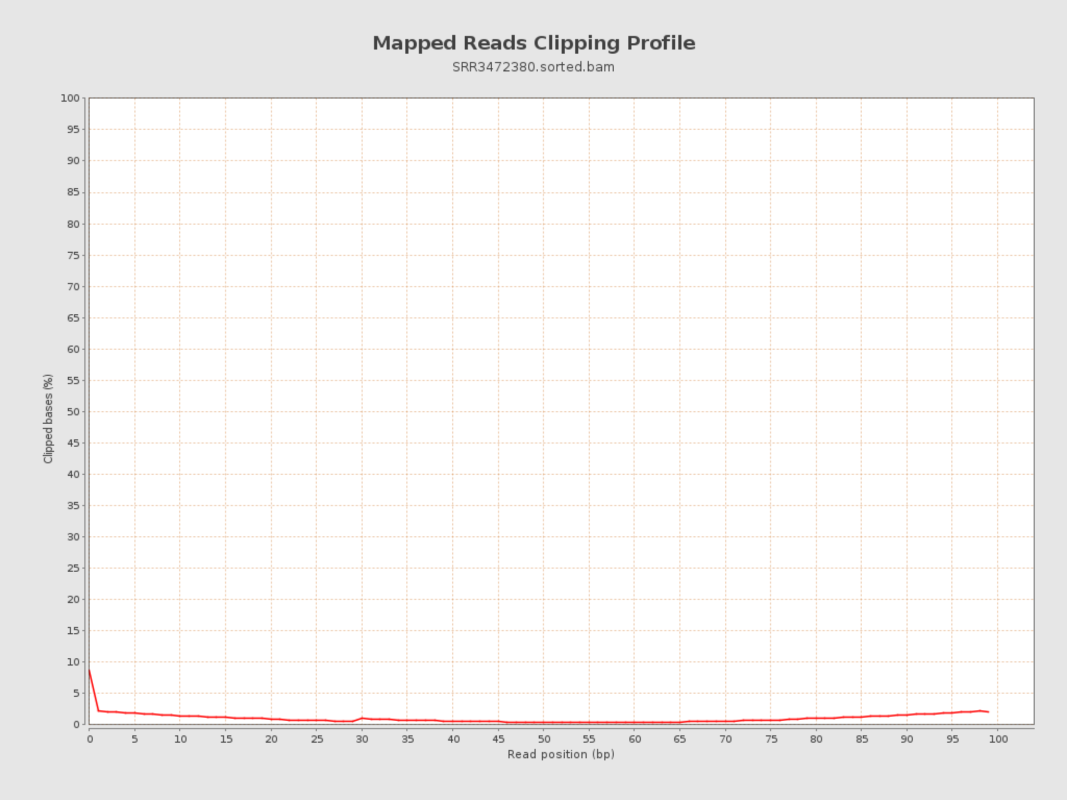
8. Results : Mapped Reads Nucleotide Content



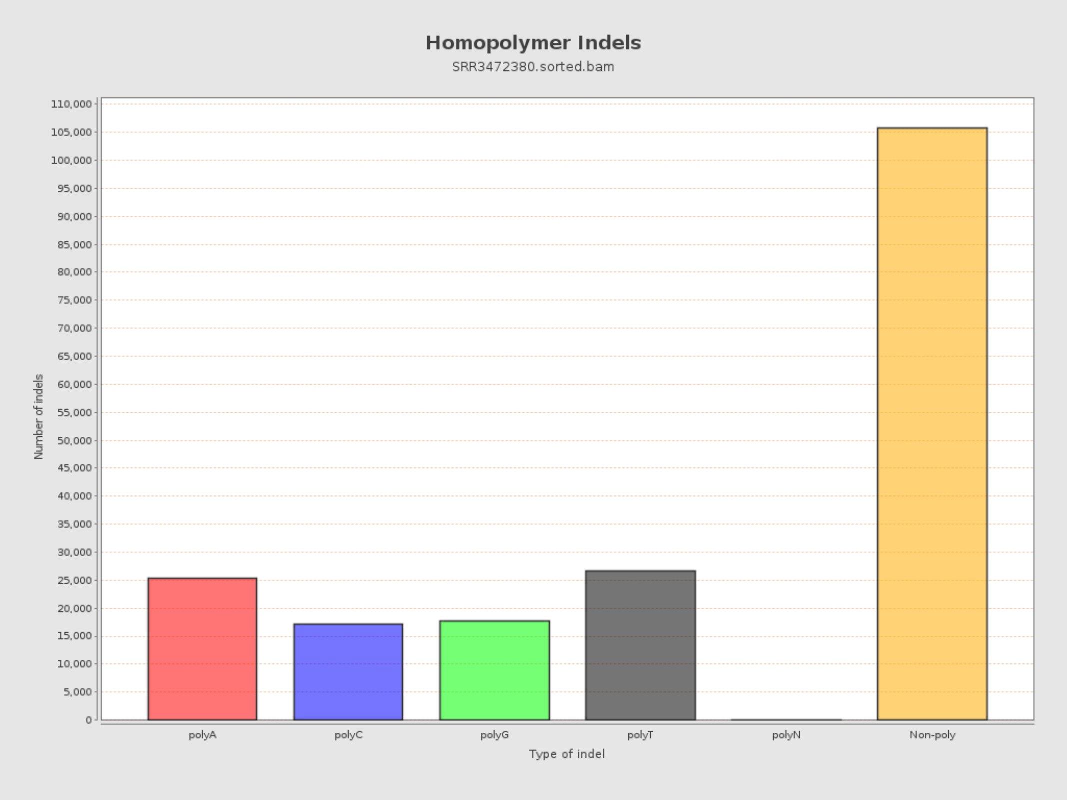
9. Results : Mapped Reads GC-content Distribution



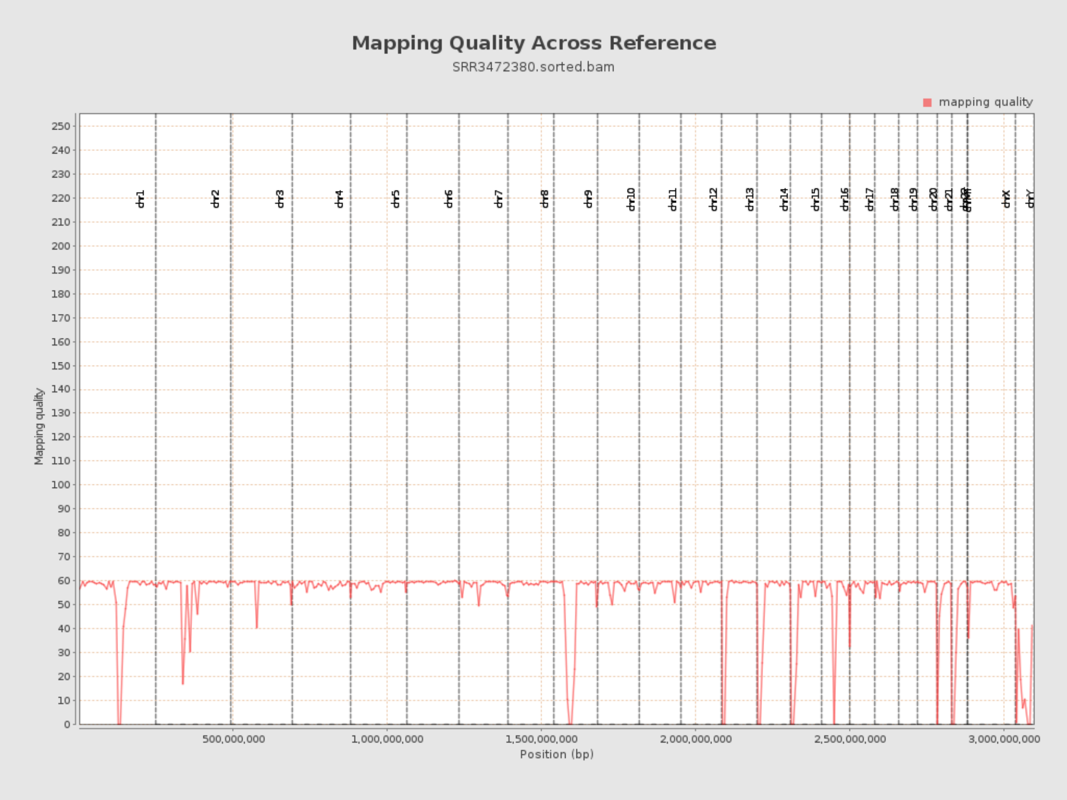
10. Results : Mapped Reads Clipping Profile



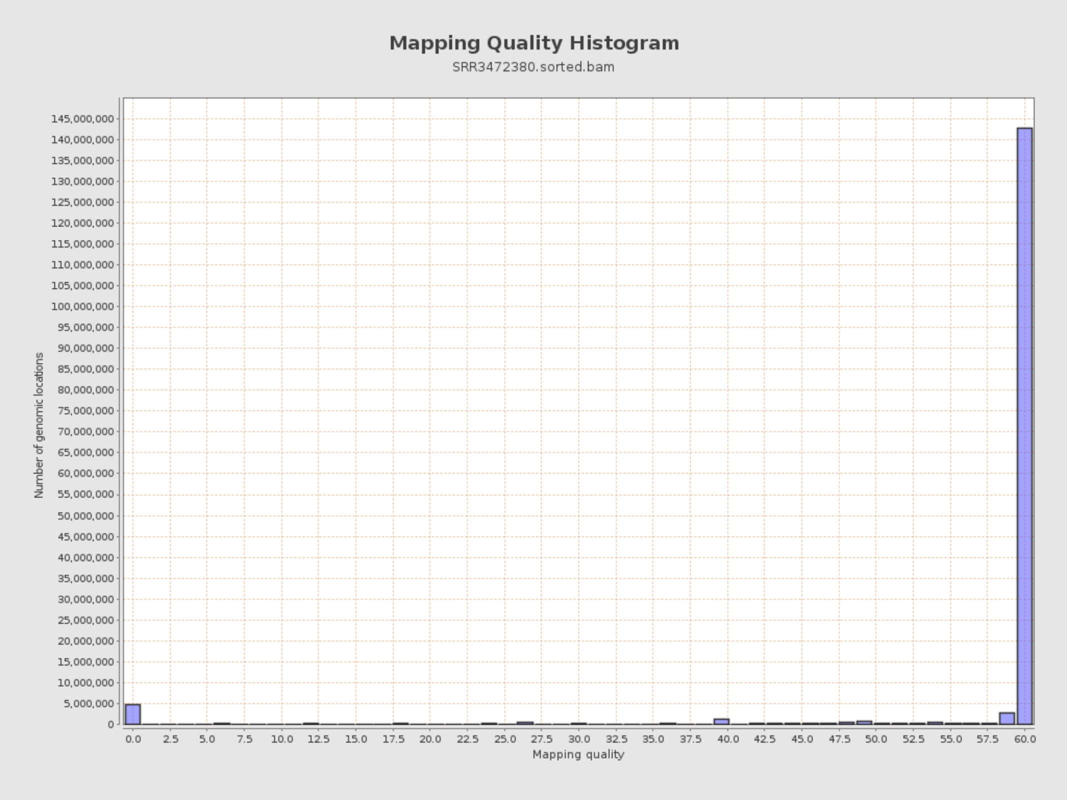
11. Results : Homopolymer Indels



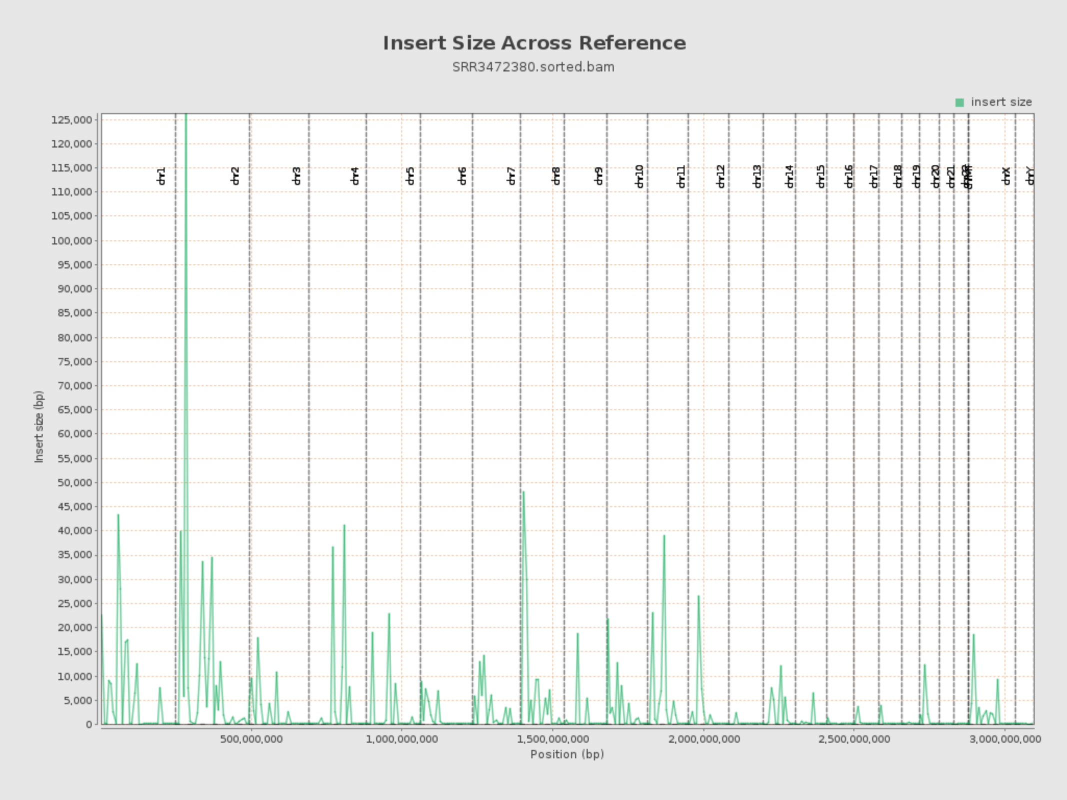
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram